

OM protein - protein search, using sw model

Run on: August 2, 2004, 08:47:48 ; Search time 54 Seconds
(without alignments)
2354.563 Million cell updates/sec

Title: US-10-015-822A-374
Perfect score: 2323
Sequence: 1 MLVTAYLAFVGLLASCLGLE.....RHDAELRVPSPTTEEPYAPEL 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2323	100.0	450	3	AAY87286	Aay87286 Human sig
2	2323	100.0	450	3	AAY99448	Aay99448 Human PRO
3	2323	100.0	450	4	AAB66197	Aab66197 Protein o
4	2323	100.0	450	4	AAG81314	Aag81314 Human AFP
5	2323	100.0	450	5	AAU86142	Aau86142 Human PRO
6	2323	100.0	450	6	ABO33690	Abo33690 Novel hum
7	2323	100.0	450	7	ABO44543	Abo44543 Human sec
8	2323	100.0	450	7	ABO33567	Abo33567 Novel hum
9	2323	100.0	450	7	ADC18243	Adc18243 Human PRO

10	2323	100.0	450	7	ADD19305	Add19305	Human	sec
11	2323	100.0	450	7	ADD70889	Add70889	Human	sec
12	2323	100.0	450	7	ADD39966	Add39966	Human	sec
13	2323	100.0	450	7	ADD70412	Add70412	Human	sec
14	2323	100.0	450	7	ADD38533	Add38533	Human	sec
15	2323	100.0	450	7	ADD39489	Add39489	Human	sec
16	2323	100.0	450	7	ADD39012	Add39012	Human	sec
17	2323	100.0	450	7	ADD40443	Add40443	Human	sec
18	2323	100.0	450	7	ADE50664	Ade50664	Human	sec
19	2323	100.0	450	7	ADE20276	Ade20276	Human	sec
20	2323	100.0	450	7	ADE50187	Ade50187	Human	sec
21	2323	100.0	450	7	ADE21745	Ade21745	Human	sec
22	2323	100.0	509	4	AAM39658	Aam39658	Human	pol
23	2323	100.0	511	4	AAM41444	Aam41444	Human	pol
24	2319	99.8	450	4	AAM93288	Aam93288	Human	pol
25	747	32.2	154	2	AAY30848	Aay30848	Human	sec
26	734	31.6	456	3	AAG35739	Aag35739	Zea	mays
27	734	31.6	474	3	AAG35738	Aag35738	Zea	mays
28	715	30.8	458	3	AAG44661	Aag44661	Zea	mays
29	714	30.7	458	3	AAG34333	Aag34333	Zea	mays
30	714	30.7	513	3	AAG34332	Aag34332	Zea	mays
31	711.5	30.6	460	3	AAG13576	Aag13576	Arabidops	
32	702	30.2	522	3	AAG42076	Aag42076	Arabidops	
33	695.5	29.9	460	3	AAG24230	Aag24230	Arabidops	
34	690	29.7	134	7	ADD19267	Add19267	Human	sec
35	684	29.4	474	3	AAG53875	Aag53875	Arabidops	
36	682.5	29.4	449	3	AAG24231	Aag24231	Arabidops	
37	680.5	29.3	408	3	AAG35740	Aag35740	Zea	mays
38	677.5	29.2	420	3	AAG31389	Aag31389	Arabidops	
39	677	29.1	411	3	AAG13578	Aag13578	Arabidops	
40	677	29.1	412	3	AAG13577	Aag13577	Arabidops	
41	671	28.9	463	3	AAG53876	Aag53876	Arabidops	
42	668.5	28.8	409	3	AAG44663	Aag44663	Zea	mays
43	668.5	28.8	410	3	AAG44662	Aag44662	Zea	mays
44	667.5	28.7	410	3	AAG34334	Aag34334	Zea	mays
45	658	28.3	412	3	AAG24232	Aag24232	Arabidops	
46	654.5	28.2	482	5	ABB92600	Abb92600	Herbicida	
47	652.5	28.1	473	3	AAG42078	Aag42078	Arabidops	
48	652.5	28.1	474	3	AAG42077	Aag42077	Arabidops	
49	646.5	27.8	426	3	AAG53877	Aag53877	Arabidops	
50	643	27.7	371	3	AAG31391	Aag31391	Arabidops	
51	643	27.7	372	3	AAG31390	Aag31390	Arabidops	
52	639	27.5	125	7	ADD19306	Add19306	Human	sec
53	449.5	19.3	247	3	AAG53908	Aag53908	Arabidops	
54	436.5	18.8	236	3	AAG53909	Aag53909	Arabidops	
55	412	17.7	199	3	AAG53910	Aag53910	Arabidops	
56	352	15.2	184	3	AAG55075	Aag55075	Arabidops	
57	186.5	8.0	129	3	AAG56688	Aag56688	Arabidops	
58	144	6.2	633	6	ABU36920	Abu36920	Protein	e
59	141	6.1	633	6	ABU34868	Abu34868	Protein	e
60	137	5.9	80	3	AAG56690	Aag56690	Arabidops	
61	137	5.9	81	3	AAG56689	Aag56689	Arabidops	
62	130	5.6	472	4	ABB66583	Abb66583	Drosophil	
63	129	5.6	474	6	ABM67264	Abm67264	Phototrab	
64	129	5.6	552	6	ABU22677	Abu22677	Protein	e
65	125.5	5.4	522	5	ABU65065	Abu65065	Human	NOV
66	124	5.3	398	6	ABU49782	Abu49782	Protein	e

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OM protein - protein search, using sw model

Run on: August 2, 2004, 08:51:18 ; Search time 17 Seconds
(without alignments)
2546.246 Million cell updates/sec

Title: US-10-015-822A-374
Perfect score: 2323
Sequence: 1 MLVTAYLAFVGLLASCLGLE.....RHDAELRVPSPTTEEPYAPEL 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	677.5	29.2	420	2	T05877	hypothetical prote
2	654.5	28.2	482	2	T45836	hypothetical prote
3	158	6.8	471	2	D83388	probable MFS trans
4	147	6.3	391	2	G83938	hypothetical prote
5	146.5	6.3	402	1	S23860	chloramphenicol re
6	145.5	6.3	587	2	T02829	conserved hypothet
7	144	6.2	633	2	B70946	NADH2 dehydrogenas
8	136.5	5.9	409	2	C82644	transcription regu
9	134.5	5.8	456	2	G83449	probable MFS trans
10	132	5.7	394	2	T31121	hypothetical prote
11	131	5.6	431	2	D81282	probable efflux pr
12	130	5.6	444	2	G83502	probable MFS trans
13	129.5	5.6	529	2	A83308	probable MFS trans

14	127.5	5.5	418	2	E72776	hypothetical prote
15	127.5	5.5	483	2	A90176	NADH dehydrogenase
16	127.5	5.5	509	2	A32101	glucose transport
17	127	5.5	452	2	S77040	hypothetical prote
18	126.5	5.4	379	2	D82481	multidrug resistanc
19	125.5	5.4	434	2	AC2833	hypothetical prote
20	125.5	5.4	434	2	G97610	hypothetical metab
21	125.5	5.4	460	2	F83639	hypothetical prote
22	125	5.4	403	2	E83408	probable MFS trans
23	124	5.3	398	2	AF0049	probable membrane
24	122	5.3	508	2	B30310	glucose transport
25	122	5.3	961	2	T03467	NADH dehydrogenase
26	121.5	5.2	417	2	B83357	probable MFS trans
27	121	5.2	509	2	A33801	muscle-fat glucose
28	120.5	5.2	792	2	A84308	chloride channel [
29	120.5	5.2	866	2	AF2886	conserved hypothet
30	120.5	5.2	866	2	C97662	hypothetical prote
31	120	5.2	403	2	B86762	hypothetical prote
32	120	5.2	411	2	A87390	transporter, proba
33	120	5.2	452	2	AI0779	probable n-hydroxy
34	119	5.1	399	2	AC2785	MFS permease [drug
35	119	5.1	399	2	D97564	hypothetical prote
36	117	5.0	568	2	JC7911	Na+-coupled citrat
37	116	5.0	419	2	B91169	probable transport
38	116	5.0	419	2	B86015	probable transport
39	116	5.0	466	1	YTBSMA	methylenomycin A r
40	116	5.0	535	2	S76103	hypothetical prote
41	115.5	5.0	484	2	T36538	probable transmemb
42	115.5	5.0	620	1	QQECD	glutathione-regula
43	115	5.0	384	2	B82420	conserved hypothet
44	115	5.0	440	2	T51556	sugar transporter-
45	114	4.9	506	2	AH3046	MFS permease [impo
46	114	4.9	506	2	D98239	probable integral
47	113.5	4.9	266	2	AI3077	hypothetical prote
48	113.5	4.9	266	2	H98208	probable permease
49	113.5	4.9	441	2	A83370	probable MFS trans
50	113.5	4.9	459	2	AE0679	probable membrane
51	113.5	4.9	477	2	G87375	major facilitator
52	113.5	4.9	569	2	T34295	hypothetical prote
53	113	4.9	402	2	B75639	probable multidrug
54	113	4.9	433	2	H90495	metabolite transpo
55	113	4.9	443	2	F71848	probable transport
56	113	4.9	464	2	F69587	L-arabinose transp
57	112.5	4.8	400	2	C70082	multidrug-efflux t
58	112.5	4.8	440	2	S47743	probable sugar tra
59	112.5	4.8	440	2	C91179	probable transport
60	112.5	4.8	440	2	D86025	probable transport
61	112.5	4.8	447	2	B64152	conserved hypothet
62	112.5	4.8	465	2	T35712	integral membrane
63	112.5	4.8	545	2	S59143	NADH2 dehydrogenas
64	112	4.8	380	2	D82965	hypothetical prote
65	112	4.8	459	1	G69005	multidrug transpor
66	112	4.8	614	2	AI2882	MFS permease [suga
67	112	4.8	657	2	G97658	hypothetical prote
68	111.5	4.8	493	2	F96696	protein FlN21.12 [
69	111.5	4.8	525	2	B82293	MviN protein VC068
70	111	4.8	419	1	S47692	hypothetical 43.8K

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OM protein - protein search, using sw model

Run on: August 2, 2004, 08:55:54 ; Search time 47 Seconds
(without alignments)
3003.347 Million cell updates/sec

Title: US-10-015-822A-374
Perfect score: 2323
Sequence: 1 MLVTAYLAFVGLLASCLGLE.....RHDAELRVSPSPTEEPYAPEL 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	2323	100.0	450	10	US-09-946-374-374	Sequence 374, App
2	2323	100.0	450	12	US-10-006-485A-374	Sequence 374, App
3	2323	100.0	450	12	US-10-013-907A-374	Sequence 374, App
4	2323	100.0	450	12	US-10-015-499A-374	Sequence 374, App
5	2323	100.0	450	12	US-10-013-910A-374	Sequence 374, App
6	2323	100.0	450	12	US-10-211-858-30	Sequence 30, Appl
7	2323	100.0	450	12	US-10-226-254A-374	Sequence 374, App
8	2323	100.0	450	12	US-10-015-395A-374	Sequence 374, App
9	2323	100.0	450	14	US-10-006-856A-374	Sequence 374, App
10	2323	100.0	450	14	US-10-006-818A-374	Sequence 374, App
11	2323	100.0	450	14	US-10-015-393A-374	Sequence 374, App
12	2323	100.0	450	14	US-10-015-869A-374	Sequence 374, App
13	2323	100.0	450	14	US-10-012-121A-374	Sequence 374, App
14	2323	100.0	450	14	US-10-006-116A-374	Sequence 374, App
15	2323	100.0	450	14	US-10-006-117A-374	Sequence 374, App
16	2323	100.0	450	14	US-10-017-527A-374	Sequence 374, App
17	2323	100.0	450	14	US-10-013-913A-374	Sequence 374, App
18	2323	100.0	450	14	US-10-007-194A-374	Sequence 374, App
19	2323	100.0	450	14	US-10-013-430A-374	Sequence 374, App
20	2323	100.0	450	14	US-10-011-671A-374	Sequence 374, App
21	2323	100.0	450	14	US-10-012-755A-374	Sequence 374, App
22	2323	100.0	450	14	US-10-062-548-97	Sequence 97, Appl
23	2323	100.0	450	14	US-10-015-386A-374	Sequence 374, App
24	2323	100.0	450	14	US-10-011-692A-374	Sequence 374, App
25	2323	100.0	450	14	US-10-006-768A-374	Sequence 374, App
26	2323	100.0	450	14	US-10-017-610A-374	Sequence 374, App
27	2323	100.0	450	14	US-10-006-063A-374	Sequence 374, App
28	2323	100.0	450	14	US-10-020-063A-374	Sequence 374, App
29	2323	100.0	450	14	US-10-015-391A-374	Sequence 374, App
30	2323	100.0	450	14	US-10-017-407A-374	Sequence 374, App
31	2323	100.0	450	14	US-10-011-833A-374	Sequence 374, App
32	2323	100.0	450	14	US-10-006-041A-374	Sequence 374, App
33	2323	100.0	450	14	US-10-015-822A-374	Sequence 374, App
34	2323	100.0	450	14	US-10-015-387A-374	Sequence 374, App
35	2323	100.0	450	14	US-10-006-130A-374	Sequence 374, App
36	2323	100.0	450	14	US-10-006-172A-374	Sequence 374, App
37	2323	100.0	450	14	US-10-017-253A-374	Sequence 374, App
38	2323	100.0	450	14	US-10-015-392A-374	Sequence 374, App
39	2323	100.0	450	14	US-10-210-951-30	Sequence 30, Appl
40	2323	100.0	450	14	US-10-017-306A-374	Sequence 374, App
41	2323	100.0	450	14	US-10-211-884-30	Sequence 30, Appl
42	2323	100.0	450	14	US-10-017-867A-374	Sequence 374, App
43	2323	100.0	450	14	US-10-012-064A-374	Sequence 374, App
44	2323	100.0	450	14	US-10-013-909A-374	Sequence 374, App
45	2323	100.0	450	14	US-10-015-671A-374	Sequence 374, App
46	2323	100.0	450	14	US-10-015-610A-374	Sequence 374, App
47	2323	100.0	450	14	US-10-012-137A-374	Sequence 374, App
48	2323	100.0	450	14	US-10-012-752A-374	Sequence 374, App
49	2323	100.0	450	14	US-10-012-754A-374	Sequence 374, App
50	2323	100.0	450	14	US-10-013-911A-374	Sequence 374, App
51	2323	100.0	450	14	US-10-013-912A-374	Sequence 374, App
52	2323	100.0	450	14	US-10-015-653A-374	Sequence 374, App
53	2323	100.0	450	14	US-10-012-101B-374	Sequence 374, App
54	2323	100.0	450	14	US-10-015-480A-374	Sequence 374, App
55	2323	100.0	450	14	US-10-015-715A-374	Sequence 374, App
56	2323	100.0	450	14	US-10-012-237A-374	Sequence 374, App

57	2323	100.0	450	14	US-10-013-906A-374	Sequence 374, App
58	2323	100.0	450	14	US-10-015-388A-374	Sequence 374, App
59	2323	100.0	450	14	US-10-012-753A-374	Sequence 374, App
60	2323	100.0	450	14	US-10-015-385A-374	Sequence 374, App
61	2323	100.0	450	14	US-10-007-236A-374	Sequence 374, App
62	2323	100.0	450	14	US-10-015-389A-374	Sequence 374, App
63	2323	100.0	450	15	US-10-015-519A-374	Sequence 374, App
64	2323	100.0	450	15	US-10-013-915A-374	Sequence 374, App
65	2323	100.0	450	15	US-10-015-394A-374	Sequence 374, App
66	2323	100.0	450	15	US-10-015-390A-374	Sequence 374, App
67	2323	100.0	450	15	US-10-006-746A-374	Sequence 374, App
68	2323	100.0	450	15	US-10-011-795A-374	Sequence 374, App
69	2323	100.0	450	15	US-10-012-231A-374	Sequence 374, App
70	2323	100.0	508	14	US-10-062-548-167	Sequence 167, App
71	1580	68.0	431	15	US-10-108-260A-4455	Sequence 4455, Ap
72	747	32.2	153	14	US-10-062-548-166	Sequence 166, App
73	747	32.2	154	14	US-10-062-548-108	Sequence 108, App
74	736	31.7	472	16	US-10-437-963-143833	Sequence 143833,
75	723	31.1	457	16	US-10-437-963-187741	Sequence 187741,
76	715	30.8	470	12	US-10-425-114-64776	Sequence 64776, A
77	694.5	29.9	459	12	US-10-424-599-230199	Sequence 230199,
78	553.5	23.8	365	12	US-10-425-114-56634	Sequence 56634, A
79	438.5	18.9	322	12	US-10-425-114-51002	Sequence 51002, A
80	331.5	14.3	179	12	US-10-424-599-230196	Sequence 230196,
81	149.5	6.4	191	12	US-10-424-599-207143	Sequence 207143,
82	144	6.2	633	12	US-10-282-122A-64844	Sequence 64844, A
83	141	6.1	633	12	US-10-282-122A-62792	Sequence 62792, A
84	140.5	6.0	440	16	US-10-437-963-143423	Sequence 143423,
85	139	6.0	285	12	US-10-425-114-54884	Sequence 54884, A
86	130	5.6	111	12	US-10-424-599-154243	Sequence 154243,
87	129	5.6	552	12	US-10-282-122A-50601	Sequence 50601, A
88	127	5.5	518	16	US-10-437-963-141943	Sequence 141943,
89	126.5	5.4	450	12	US-10-424-599-199544	Sequence 199544,
90	125.5	5.4	522	12	US-10-092-900A-50	Sequence 50, Appl
91	125.5	5.4	522	12	US-10-403-161-74	Sequence 74, Appl
92	124	5.3	398	12	US-10-282-122A-77706	Sequence 77706, A
93	124	5.3	628	12	US-10-282-122A-62000	Sequence 62000, A
94	123	5.3	440	15	US-10-085-198-114	Sequence 114, App
95	122.5	5.3	427	12	US-10-282-122A-43406	Sequence 43406, A
96	121.5	5.2	405	12	US-10-282-122A-60023	Sequence 60023, A
97	121.5	5.2	524	12	US-10-425-114-71863	Sequence 71863, A
98	121	5.2	509	9	US-09-981-947A-6	Sequence 6, Appli
99	120	5.2	464	12	US-10-282-122A-71751	Sequence 71751, A
100	118.5	5.1	554	16	US-10-437-963-141947	Sequence 141947,
101	118	5.1	593	14	US-10-222-009-27	Sequence 27, Appl
102	118	5.1	610	14	US-10-222-009-10	Sequence 10, Appl
103	117	5.0	430	14	US-10-156-761-10694	Sequence 10694, A
104	117	5.0	488	9	US-09-790-099-2	Sequence 2, Appli
105	117	5.0	488	14	US-10-237-852-2	Sequence 2, Appli
106	116.5	5.0	402	12	US-10-282-122A-55712	Sequence 55712, A
107	116.5	5.0	411	14	US-10-156-761-10140	Sequence 10140, A
108	116.5	5.0	437	12	US-10-282-122A-50397	Sequence 50397, A
109	116	5.0	539	15	US-10-310-154-723	Sequence 723, App
110	116	5.0	571	13	US-10-051-909-34	Sequence 34, Appl
111	115	5.0	418	12	US-10-282-122A-69671	Sequence 69671, A
112	114.5	4.9	373	12	US-10-282-122A-47451	Sequence 47451, A
113	114.5	4.9	424	12	US-10-282-122A-62145	Sequence 62145, A

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OM protein - protein search, using sw model

Run on: August 2, 2004, 08:53:33 ; Search time 19 Seconds
(without alignments)
1222.720 Million cell updates/sec

Title: US-10-015-822A-374
Perfect score: 2323
Sequence: 1 MLVTAYLAFVGLLASCLGLE.....RHDAELRVSPTEEPYAPEL 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result						Description
	No.	Score	Match	Length	ID	
			%	DB		
			Query			
1	2323	100.0	450	4	US-09-369-247-97	Sequence 97, Appl
2	2323	100.0	508	4	US-09-369-247-167	Sequence 167, App
3	747	32.2	153	4	US-09-369-247-166	Sequence 166, App
4	747	32.2	154	4	US-09-369-247-108	Sequence 108, App
5	158	6.8	502	4	US-09-252-991A-24948	Sequence 24948, A
6	132.5	5.7	529	4	US-09-252-991A-19364	Sequence 19364, A
7	129.5	5.6	664	4	US-09-252-991A-31745	Sequence 31745, A
8	125.5	5.4	517	4	US-09-252-991A-21762	Sequence 21762, A
9	125.5	5.4	717	4	US-09-252-991A-25715	Sequence 25715, A
10	123.5	5.3	466	4	US-09-134-001C-3526	Sequence 3526, Ap
11	122	5.3	313	4	US-09-252-991A-32017	Sequence 32017, A

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OM protein - protein search, using sw model

Run on: August 2, 2004, 08:50:28 ; Search time 39 Seconds
 (without alignments)
 3640.595 Million cell updates/sec

Title: US-10-015-822A-374
 Perfect score: 2323
 Sequence: 1 MLVTAYLAFVGLLASCLGLE.....RHDAELRVPSPTTEEPYAPEL 450

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : SPTREMBL_25:*
 1: sp_archaea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phage:*
 10: sp_plant:*
 11: sp_rodent:*
 12: sp_virus:*
 13: sp_vertibrate:*
 14: sp_unclassified:*
 15: sp_rvirus:*
 16: sp_bacteriap:*
 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	2323	100.0	450	4	Q96IA5	Q96ia5 homo sapien
2	2319	99.8	450	4	Q8NCK0	Q8nck0 homo sapien
3	2253	97.0	450	11	Q921Y4	Q921y4 mus musculu
4	1580	68.0	431	4	Q8N7W8	Q8n7w8 homo sapien
5	728	31.3	456	10	Q9FWD6	Q9fwd6 oryza sativ
6	728	31.3	456	10	Q7XCQ6	Q7xcq6 oryza sativ
7	723	31.1	457	10	Q8GZW6	Q8gzw6 oryza sativ
8	711.5	30.6	460	10	Q9C5R0	Q9c5r0 arabidopsis
9	696.5	30.0	460	10	Q9CA11	Q9ca11 arabidopsis
10	693.5	29.9	474	10	Q9SGV0	Q9sgv0 arabidopsis
11	677.5	29.2	420	10	Q9T094	Q9t094 arabidopsis
12	654.5	28.2	482	10	Q9M3A1	Q9m3a1 arabidopsis
13	630.5	27.1	432	5	Q9N3A9	Q9n3a9 caenorhabdi
14	242	10.4	449	10	Q8GXH4	Q8gxh4 arabidopsis
15	182	7.8	399	16	Q8RCM8	Q8rcm8 thermoanaer
16	158	6.8	471	16	Q9I260	Q9i260 pseudomonas
17	150.5	6.5	408	16	Q7WK07	Q7wk07 bordetella
18	147	6.3	391	16	Q9KAH6	Q9kah6 bacillus ha
19	147	6.3	441	16	Q8XQK1	Q8xqk1 ralstonia s
20	147	6.3	447	16	Q7UR67	Q7ur67 rhodopirell
21	145.5	6.3	587	5	O00904	O00904 leishmania
22	141.5	6.1	511	16	Q83C84	Q83c84 coxiella bu
23	141	6.1	402	2	Q9LA76	Q9la76 streptomyce
24	141	6.1	633	16	Q7TX55	Q7tx55 mycobacteri
25	139	6.0	497	16	Q98M07	Q98m07 rhizobium l
26	136.5	5.9	409	16	Q9PCM9	Q9pcm9 xylella fas
27	136	5.9	475	16	Q8XWZ4	Q8xwz4 ralstonia s
28	135.5	5.8	423	16	Q8EEK8	Q8EEK8 shewanella
29	134.5	5.8	456	16	Q9I3E8	Q9i3e8 pseudomonas
30	133.5	5.7	414	16	Q880J8	Q880j8 pseudomonas
31	133	5.7	431	2	Q9ZF64	Q9zf64 campylobact
32	132	5.7	394	2	O85830	O85830 sphingomona
33	131.5	5.7	460	16	Q89ZI0	Q89zi0 bacteroides
34	131	5.6	431	16	Q9PMS5	Q9pms5 campylobact
35	130	5.6	444	16	Q9I4J1	Q9i4j1 pseudomonas
36	130	5.6	491	5	Q9U622	Q9u622 drosophila
37	129.5	5.6	408	16	Q7WJJ6	Q7wjj6 bordetella
38	129.5	5.6	408	16	Q7WAF3	Q7waf3 bordetella
39	129.5	5.6	408	16	Q7VWT5	Q7vwt5 bordetella
40	129.5	5.6	458	16	Q8CQD3	Q8cqd3 staphylococ
41	129.5	5.6	529	16	Q9I0E1	Q9i0e1 pseudomonas
42	127.5	5.5	418	17	Q9YFQ0	Q9yfq0 aeropyrum p
43	127.5	5.5	428	16	Q83E95	Q83e95 coxiella bu
44	127.5	5.5	483	17	Q980G8	Q980g8 sulfolobus
45	127	5.5	452	16	Q55962	Q55962 synechocyst
46	126.5	5.4	379	16	Q9KMQ3	Q9kmq3 vibrio chol
47	125.5	5.4	434	16	Q8UDN2	Q8udn2 agrobacteri
48	125.5	5.4	440	16	Q8KG66	Q8kg66 chlorobium
49	125.5	5.4	460	16	Q9I789	Q9i789 pseudomonas
50	125	5.4	403	16	Q9I2J6	Q9i2j6 pseudomonas
51	124	5.3	398	16	Q8ZIT9	Q8zit9 yersinia pe
52	123.5	5.3	400	16	Q8RAQ6	Q8raq6 thermoanaer
53	123.5	5.3	516	11	Q8CE47	Q8ce47 mus musculu
54	123	5.3	400	16	Q82SH9	Q82sh9 nitrosomona
55	123	5.3	448	16	Q89RS1	Q89rs1 bradyrhizob
56	123	5.3	502	16	Q98B85	Q98b85 rhizobium l
57	122.5	5.3	504	16	Q87X88	Q87x88 pseudomonas

OM protein - protein search, using sw model

Run on: August 2, 2004, 08:49:38 ; Search time 14 Seconds
(without alignments)
1673.684 Million cell updates/sec

Title: US-10-015-822A-374
Perfect score: 2323
Sequence: 1 MLVTAYLAFVGLLASCLGLE.....RHDAELRVSPTEEPYAPEL 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	146.5	6.3	402	1	OPDE_PSEAE Q01602 pseudomonas
2	144	6.2	633	1	NUOL_MYCTU O86350 mycobacteri
3	127.5	5.5	509	1	GTR4_RAT P19357 rattus norv
4	121	5.2	509	1	GTR4_HUMAN P14672 homo sapien
5	121	5.2	509	1	GTR4_MOUSE P14142 mus musculu
6	116	5.0	419	1	YHHS_ECO57 Q8x6p4 escherichia
7	116	5.0	466	1	MMR_BACSU Q00538 bacillus su
8	115.5	5.0	620	1	KEFC_ECOLI P03819 escherichia
9	114.5	4.9	620	1	KEFC_ECOL6 Q8fla1 escherichia
10	113	4.9	464	1	ARAE_BACSU P96710 bacillus su
11	113	4.9	509	1	GTR4_BOVIN Q27994 bos taurus
12	112.5	4.8	440	1	YHJE_ECOLI P37643 escherichia
13	112.5	4.8	447	1	Y418_HAEIN P44699 haemophilus
14	112.5	4.8	545	1	NU5M_ALBCO P48918 albinaria c
15	112	4.8	1108	1	EMBA_MYCAV P71485 mycobacteri
16	111.5	4.8	419	1	YHHS_SALTY Q8zle4 salmonella
17	111.5	4.8	525	1	MVIN_VIBCH O34238 vibrio chol